



SEQUENCE LISTING

<110> Hayward, Nicholas K.
Weber, Gunther
Grimmond, Sean
Nordenskjold, Magnus
Larsson, Catharina

<120> A NOVEL GROWTH FACTOR AND A GENETIC SEQUENCE ENCODING SAME

<130> Dav. Col. Cave

<140> 09/349,954
<141> 1999-07-08

<150> 08/765,588
<151> 1996-02-22

<160> 22

<170> PatentIn Ver. 2.1

<210> 1
<211> 649
<212> DNA
<213> Nucleotide Sequence of VEGF165

<220>
<221> CDS
<222> (17)..(589)

<400> 1
tcgggcctcc gaaacc atg aac ttt ctg ctg tct tgg gtg cat tgg agc ctt 52

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu
1 5 10

gcc ttg ctg ctc tac ctc cac cat gcc aag tgg tcc cag gct gca ccc 100

Ala Leu Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro
15 20 25

atg gca gaa gga gga ggg cag aat cat cac gaa gtg gtg aag ttc atg 148

Met Ala Glu Gly Gly Gln Asn His His Glu Val Val Lys Phe Met
30 35 40

gat gtc tat cag cgc agc tac tgc cat cca atc gag acc ctg gtg gac 196

Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp
45 50 55 60

atc ttc cag gag tac cct gat gag atc gag tac atc ttc aag cca tcc 244

Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser			
65	70	75	
tgt gtg ccc ctg atg cga tgc ggg ggc tgc tgc aat gac gag ggc ctg			292
Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu			
80	85	90	
gag tgt gtg ccc act gag gag tcc aac atc acc atg cag att atg cg			340
Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg			
95	100	105	
atc aaa cct cac caa ggc cag cac ata gga gag atg agc ttc cta cag			388
Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln			
110	115	120	
cac aac aaa tgt gaa tgc aga cca aag aaa gat aga gca aga caa gaa			436
His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu			
125	130	135	140
aat ccc tgt ggg cct tgc tca gag cgg aga aag cat ttg ttt gta caa			484
Asn Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln			
145	150	155	
gat ccg cag acg tgt aaa tgt tcc tgc aaa aac aca gac tcg cgt tgc			532
Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys			
160	165	170	
aag gcg agg cag ctt gag tta aac gaa cgt act tgc aga tgt gac aag			580
Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys			
175	180	185	
ccg agg cgg tgagccgggc aggaggaagg agcctccctc agcgtttcgg			629
Pro Arg Arg			
190			
gaaccagatc tctcaccagg			649

<210> 2
 <211> 191
 <212> PRT
 <213> Nucleotide Sequence of VEGF165

 <400> 2
 Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
 1 5 10 15

Tyr	Leu	His	His	Ala	Lys	Trp	Ser	Gln	Ala	Ala	Pro	Met	Ala	Glu	Gly
				20				25						30	
Gly	Gly	Gln	Asn	His	His	Glu	Val	Val	Lys	Phe	Met	Asp	Val	Tyr	Gln
		35				40							45		
Arg	Ser	Tyr	Cys	His	Pro	Ile	Glu	Thr	Leu	Val	Asp	Ile	Phe	Gln	Glu
				50		55					60				
Tyr	Pro	Asp	Glu	Ile	Glu	Tyr	Ile	Phe	Lys	Pro	Ser	Cys	Val	Pro	Leu
	65				70				75					80	
Met	Arg	Cys	Gly	Gly	Cys	Cys	Asn	Asp	Glu	Gly	Leu	Glu	Cys	Val	Pro
				85				90					95		
Thr	Glu	Glu	Ser	Asn	Ile	Thr	Met	Gln	Ile	Met	Arg	Ile	Lys	Pro	His
	100						105						110		
Gln	Gly	Gln	His	Ile	Gly	Glu	Met	Ser	Phe	Leu	Gln	His	Asn	Lys	Cys
	115					120					125				
Glu	Cys	Arg	Pro	Lys	Lys	Asp	Arg	Ala	Arg	Gln	Glu	Asn	Pro	Cys	Gly
	130					135					140				
Pro	Cys	Ser	Glu	Arg	Arg	Lys	His	Leu	Phe	Val	Gln	Asp	Pro	Gln	Thr
	145					150				155				160	
Cys	Lys	Cys	Ser	Cys	Lys	Asn	Thr	Asp	Ser	Arg	Cys	Lys	Ala	Arg	Gln
					165				170				175		
Leu	Glu	Leu	Asn	Glu	Arg	Thr	Cys	Arg	Cys	Asp	Lys	Pro	Arg	Arg	
				180				185					190		

<210> 3
<211> 1094
<212> DNA
<213> Nucleotide Sequence of SOM175

<220>
<221> CDS
<222> (3)..(623)

<400> 3
cc atg agc cct ctg ctc cgc cgc ctg ctg ctc gcc gca ctc ctg cag 47
Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln
1 5 10 15
ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95
Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His
20 25 30

cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc	143
Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys	
35 40 45	
cag ccc cg ^g gag gtg gtg ccc ttg act gtg gag ctc atg ggc acc	191
Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr	
50 55 60	
gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt	239
Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly	
65 70 75	
ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac	287
Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His	
80 85 90 95	
caa gtc cg ^g atg cag atc ctc atg atc cg ^g tac ccg agc agt cag ctg	335
Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu	
100 105 110	
ggg gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa	383
Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys	
115 120 125	
aaa aag gac agt gct gtg aag cca gac agg gct gcc act ccc cac cac	431
Lys Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His	
130 135 140	
cgt ccc cag ccc cgt tct gtt ccg ggc tgg gac tct gcc ccc gga gca	479
Arg Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala	
145 150 155	
ccc tcc cca gct gac atc acc cat ccc act cca gcc cca ggc ccc tct	527
Pro Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser	
160 165 170 175	
gcc cac gct gca ccc agc acc acc agc gcc ctg acc ccc gga cct gcc	575
Ala His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala	
180 185 190	
gct gcc gct gcc gac gcc gca gct tcc tcc gtt gcc aag ggc ggg gct	623
Ala Ala Ala Ala Asp Ala Ala Ser Ser Val Ala Lys Gly Gly Ala	
195 200 205	

tagagctcaa cccagacacc tgcaggtgcc ggaagctgcg aaggtgacac atggctttc 683
agactcagca gggtgacttg cctcagaggc tatatcccag tgggggaaca aaggggagcc 743
tggtaaaaaaa cagccaagcc cccaagacct cagcccaggc agaagctgct ctaggacctg 803
ggcctctcaag aggctcttc tgccatccct tgtctccctg aggccatcat caaacaggac 863
agagttggaa gaggagactg ggaggcagca agaggggtca cataccagct caggggagaa 923
tggagtactg tctcagtttc taaccactct gtgcaagtaa gcattttaca actggcttt 983
cctccccca ctaagaagac ccaaacctct gcataatggg atttgggctt tggtacaaga 1043
actgtgaccc ccaaccctga taaaagagat ggaaggaaaa aaaaaaaaaa a 1094

<210> 4

<211> 207

<212> PRT

<213> Nucleotide Sequence of SOM175

<400> 4

Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu
1 5 10 15

Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
20 25 30

Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
35 40 45

Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
50 55 60

Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
65 70 75 80

Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
85 90 95

Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
100 105 110

Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
115 120 125

Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg

130	135	140
Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro		
145	150	155
Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser Ala		
165	170	175
His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala Ala		
180	185	190
Ala Ala Ala Asp Ala Ala Ser Ser Val Ala Lys Gly Gly Ala		
195	200	205
<210> 5		
<211> 993		
<212> DNA		
<213> Nuc. Seq. of SOM175 Absent Exon 6		
<220>		
<221> CDS		
<222> (3)..(566)		
<400> 5		
cc atg agc cct ctg ctc cgc cgc ctg ctg ctc gcc gca ctc ctg cag		47
Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln		
1	5	10
ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac		95
Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His		
20	25	30
cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc		143
Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys		
35	40	45
cag ccc cgg gag gtg gtg ccc ttg act gtg gag ctc atg ggc acc		191
Gln Pro Arg Glu Val Val Pro Leu Thr Val Glu Leu Met Gly Thr		
50	55	60
gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt		239
Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly		
65	70	75
ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac		287
Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His		
80	85	90
95		

caa gtc cg_g atg cag atc ctc atg atc cg_g tac cc_g agc agt cag ctg 335
 Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu
 100 105 110
 ggg gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa 383
 Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys
 115 120 125
 aaa aag gac agt gct gtg aag cca gat agc ccc agg ccc ctc tgc cca 431
 Lys Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro
 130 135 140
 cg_c tgc acc cag cac cac cag cg_c cct gac ccc cg_g acc tgc cg_c tgc 479
 Arg Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys
 145 150 155
 cg_c tgc cga cg_c cg_c agc ttc ctc cgt tgc caa ggg cg_g ggc tta gag 527
 Arg Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu
 160 165 170 175
 ctc aac cca gac acc tgc agg tgc cg_g aag ctg cga agg tgacacatgg 576
 Leu Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg
 180 185
 cttttcagac tcagcgagggt gacttgctc agaggctata tcccagtggg ggaacaaagg 636

 ggagcctgggt aaaaaacagc caagccccca agacctcagc ccaggcagaa gctgctctag 696

 gacctgggcc tctcagaggg ctcttctgcc atcccttgc tccctgaggc catcatcaa 756

 caggacagag ttggaagagg agactggag gcagcaagag gggcacata ccagctcagg 816

 ggagaatgga gtactgtctc agtttcta_ac cactctgtgc aagtaagcat cttacaactg 876

 gctcttcctc ccctcactaa gaagacccaa acctctgc_at aatggattt gggctttgg 936

 acaagaactg tgaccccaa ccctgataaa agagatggaa ggaaaaaaaaaaa aaaaaaaaaa 993

<210> 6
 <211> 188
 <212> PRT
 <213> Nuc. Seq. of SOM175 Absent Exon 6

<400> 6
 Met Ser Pro Leu Leu Arg Arg Leu Leu Ala Ala Leu Leu Gln Leu
 1 5 10 15

 Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
 20 25 30

 Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
 35 40 45

 Pro Arg Glu Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
 50 55 60

 Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
 65 70 75 80

 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
 85 90 95

 Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
 100 105 110

 Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
 115 120 125

 Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro Arg
 130 135 140

 Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys Arg
 145 150 155 160

 Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu Leu
 165 170 175

 Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg
 180 185

<210> 7
 <211> 858
 <212> DNA
 <213> Nuc. Seq. of SOM175 Absent Exons 6&7

<220>
 <221> CDS
 <222> (3)..(431)

<400> 7
 cc atg agc cct ctg ctc cgc cgc ctg ctg ctc gcc gca ctc ctg cag 47

 Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln
 1 5 10 15

 ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95

Leu	Ala	Pro	Ala	Gln	Ala	Pro	Val	Ser	Gln	Pro	Asp	Ala	Pro	Gly	His	
						20			25					30		
cag	agg	aaa	gtg	gtg	tca	tgg	ata	gat	gtg	tat	act	cgc	gct	acc	tgc	143
Gln	Arg	Lys	Val	Val	Ser	Trp	Ile	Asp	Val	Tyr	Thr	Arg	Ala	Thr	Cys	
						35			40					45		
cag	ccc	cg	gag	gtg	gtg	ccc	ttg	act	gtg	gag	ctc	atg	ggc	acc		191
Gln	Pro	Arg	Glu	Val	Val	Val	Pro	Leu	Thr	Val	Glu	Leu	Met	Gly	Thr	
						50			55				60			
gtg	gcc	aaa	cag	ctg	gtg	ccc	agc	tgc	gtg	act	gtg	cag	cgc	tgt	ggt	239
Val	Ala	Lys	Gln	Leu	Val	Pro	Ser	Cys	Val	Thr	Val	Gln	Arg	Cys	Gly	
						65			70				75			
ggc	tgc	tgc	cct	gac	gat	ggc	ctg	gag	tgt	gtg	ccc	act	ggg	cag	cac	287
Gly	Cys	Cys	Pro	Asp	Asp	Gly	Leu	Glu	Cys	Val	Pro	Thr	Gly	Gln	His	
						80			85			90		95		
caa	gtc	cg	atg	cag	atc	ctc	atg	atc	cg	tac	ccg	agc	agt	cag	ctg	335
Gln	Val	Arg	Met	Gln	Ile	Leu	Met	Ile	Arg	Tyr	Pro	Ser	Ser	Gln	Leu	
						100			105				110			
ggg	gag	atg	tcc	ctg	gaa	gaa	cac	agc	cag	tgt	gaa	tgc	aga	cct	aaa	383
Gly	Glu	Met	Ser	Leu	Glu	Glu	His	Ser	Gln	Cys	Glu	Cys	Arg	Pro	Lys	
						115			120				125			
aaa	aag	gac	agt	gct	gtg	aag	cca	gat	agg	tgc	cg	aag	ctg	cga	agg	431
Lys	Lys	Asp	Ser	Ala	Val	Lys	Pro	Asp	Arg	Cys	Arg	Lys	Leu	Arg	Arg	
						130			135			140				
tgacacatgg	ctttcagac	tcagcagggt	gacttgctc	agaggctata	tcccagtggg											491
ggaacaaagg	ggagcctggt	aaaaaacagc	caagccccca	agacctcagc	ccaggcagaa											551
gctgctctag	gacctgggcc	tctcagaggg	ctcttctgcc	atcccttgtc	tccctgaggc											611
catcatcaa	caggacagag	ttgaaagagg	agactgggag	gcagcaagag	gggtcacata											671
ccagctcagg	ggagaatgga	gtactgtctc	agtttcta	cactctgtgc	aagtaagcat											731
cttacaactg	gctcttcctc	ccctcactaa	gaagacccaa	acctctgcat	aatgggattt											791

gggcttttgtt acaagaactg tgaccccaa ccctgataaa agagatggaa ggaaaaaaaaa 851

aaaaaaaaa 858

<210> 8

<211> 143

<212> PRT

<213> Nuc. Seq. of SOM175 Absent Exons 6&7

<400> 8

Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu
1 5 10 15

Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
20 25 30

Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
35 40 45

Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
50 55 60

Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
65 70 75 80

Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
85 90 95

Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
100 105 110

Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
115 120 125

Lys Asp Ser Ala Val Lys Pro Asp Arg Cys Arg Lys Leu Arg Arg
130 135 140

<210> 9

<211> 910

<212> DNA

<213> Nuc. Seq. of SOM175 Absent Exon 4

<220>

<221> CDS

<222> (3)..(305)

<400> 9

cc atg agc cct ctg ctc cgc cgc ctg ctg ctc gcc gca ctc ctg cag 47

Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln
1 5 10 15

ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95
Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His
20 25 30
cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc 143
Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys
35 40 45
cag ccc cgg gag gtg gtg ccc ttg act gtg gag ctc atg ggc acc 191
Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr
50 55 60
gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt 239
Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly
65 70 75
ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac 287
Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His
80 85 90 95
caa gtc cgg atg cag acc taaaaaaaaag gacagtgcgtg tgaagccaga 335
Gln Val Arg Met Gln Thr
100
cagggctgcc actccccacc accgtccccca gccccgttct gttccgggct gggactctgc 395
ccccggagca ccctccccag ctgacatcac ccatcccact ccagccccag gcccctctgc 455
ccacgctgca cccagcacca ccagcgccct gaccccccga cctgcccgtg ccgctgcccga 515
cgccgcagct tcctccgttg ccaaggcggt ggcttagagc tcaacccaga cacctgcagg 575
tgccggaagc tgcaagggtg acacatggct tttcagactc agcagggtga cttgcctcag 635
aggctataatc ccagtgggaa acaaagagga gcctggtaaa aaacagccaa gcccccaaga 695
cctcagccca ggcagaagct gctctaggac ctgggcctct cagagggtct ttctgccatc 755
ccttgtctcc ctgaggccat catcaaacag gacagagttg gaagaggaga ctgggaggca 815
gcaagaggggg tcacatacca qctcagggaa gaatggagta ctgtctcagt ttctaaccac 875

tctgtgcaag taagcatctt acaaactggct cttcc 910

<210> 10
<211> 101
<212> PRT
<213> Nuc. Seq. of SOM175 Absent Exon 4

<400> 10
Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu
1 5 10 15

Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
20 25 30

Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
35 40 45

Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
50 55 60

Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
65 70 75 80

Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
85 90 95

Val Arg Met Gln Thr
100

<210> 11
<211> 42
<212> DNA
<213> Oligonucleotide

<400> 11
accaccacct ccctgggctg gcatgtggca cgtgcataaaa cg 42

<210> 12
<211> 42
<212> DNA
<213> Oligonucleotide

<400> 12
agttgttga ccacattgcc catgagttcc atgctcagag gc 42

<210> 13
<211> 38
<212> DNA

<213> Oligonucleotide

<400> 13

gatcctgggg ctggagtgaa atggatgtat tcagctgg

38

<210> 14

<211> 40

<212> DNA

<213> Oligonucleotide

<400> 14

gcgggcagag gatcctgggg ctgtctggcc tcacagcact

40

<210> 15

<211> 236

<212> DNA

<213> Human SOM175

<400> 15

atgagggggcc aggtacgtga ggtctccac aggccccctgg aaagaatact tacatctgct 60

cccatggtgt atgcagggtcc gagatgctga atacagatcc tcatgcaggt gtcaggcaac 120

ttttcaagac ctaaagacag gtgagtcttt ctcctccgtta ggctgcctcc agccccaggc 180

cccccaactcc agccccagac ccagacacct gtagccctgc tcaggtgccg aggtga 236

<210> 16

<211> 1242

<212> DNA

<213> mVRF

<220>

<221> CDS

<222> (166)..(789)

<400> 16

gcacgagctc aggccgtcg tgcggcgctg cttgcgcctg cctgcgccta gggctcgaaa 60

ggggggcccgcg gaggagccgc cccctgcgc cccgcgggggg tccccgggtc cgccatgg 120

ggcggctctg gctgacccccc ccccacacccg ccgggctagg gcccgg atg agc ccc ctg 177

Met Ser Pro Leu
1

ctg cgt cgc ctg ctg ctt gtt gca ctg ctg cag ctg gct cgc acc cag 225

Leu	Arg	Arg	Leu	Leu	Leu	Val	Ala	Leu	Leu	Gln	Leu	Ala	Arg	Thr	Gln	
5					10					15					20	
gcc	cct	gtg	tcc	cag	ttt	gat	ggc	ccc	agt	cac	cag	aag	aaa	gtg	gtg	273
Ala	Pro	Val	Ser	Gln	Phe	Asp	Gly	Pro	Ser	His	Gln	Lys	Lys	Val	Val	
				25					30					35		
cca	tgg	ata	gac	gtt	tat	gca	cgt	gcc	aca	tgc	cag	ccc	agg	gag	gtg	321
Pro	Trp	Ile	Asp	Val	Tyr	Ala	Arg	Ala	Thr	Cys	Gln	Pro	Arg	Glu	Val	
			40						45					50		
gtg	gtg	cct	ctg	agc	atg	gaa	ctc	atg	ggc	aat	gtg	gtc	aaa	caa	cta	369
Val	Val	Pro	Leu	Ser	Met	Glu	Leu	Met	Gly	Asn	Val	Val	Lys	Gln	Leu	
			55				60						65			
gtg	ccc	agc	tgt	gtg	act	gtg	cag	cgc	tgt	ggt	ggc	tgc	tgc	cct	gac	417
Val	Pro	Ser	Cys	Val	Thr	Val	Gln	Arg	Cys	Gly	Gly	Cys	Cys	Pro	Asp	
			70			75							80			
gat	ggc	ctg	gaa	tgt	gtg	ccc	act	ggg	caa	cac	caa	gtc	cga	atg	cag	465
Asp	Gly	Leu	Glu	Cys	Val	Pro	Thr	Gly	Gln	His	Gln	Val	Arg	Met	Gln	
			85			90				95					100	
atc	ctc	atg	atc	cag	tac	ccg	agc	agt	cag	ctg	ggg	gag	atg	tcc	ctg	513
Ile	Leu	Met	Ile	Gln	Tyr	Pro	Ser	Ser	Gln	Leu	Gly	Glu	Met	Ser	Leu	
			105						110					115		
gga	gaa	cac	agc	caa	tgt	gaa	tgc	aga	cct	aaa	aaa	aag	gag	agt	gct	561
Gly	Glu	His	Ser	Gln	Cys	Glu	Cys	Arg	Pro	Lys	Lys	Lys	Glu	Ser	Ala	
			120				125						130			
gtg	agg	cca	gac	agg	gtt	gcc	ata	ccc	cac	cac	cgt	ccc	cag	ccc	cgc	609
Val	Arg	Pro	Asp	Arg	Val	Ala	Ile	Pro	His	His	Arg	Pro	Gln	Pro	Arg	
			135				140						145			
tct	gtt	ccg	ggc	tgg	gac	tct	acc	ccg	gga	gca	ccc	tcc	cca	gct	gac	657
Ser	Val	Pro	Gly	Trp	Asp	Ser	Thr	Pro	Gly	Ala	Pro	Ser	Pro	Ala	Asp	
			150			155							160			
atc	atc	cat	ccc	act	cca	gcc	cca	gga	tcc	tct	gcc	cgc	ctt	gca	ccc	705
Ile	Ile	His	Pro	Thr	Pro	Ala	Pro	Gly	Ser	Ser	Ala	Arg	Leu	Ala	Pro	
			165				170			175				180		
agc	gcc	gcc	aac	gcc	ctg	acc	ccc	gga	cct	gcc	gtt	gcc	gct	gta	gac	753
Ser	Ala	Ala	Asn	Ala	Leu	Thr	Pro	Gly	Pro	Ala	Val	Ala	Ala	Val	Asp	

	185	190	195	
gcc gcc gct tcc tcc att gcc aag ggc ggg gct tag agctcaaccc				799
Ala Ala Ala Ser Ser Ile Ala Lys Gly Gly Ala				
	200	205		
agacacacctgt aggtgccgga agccgcgaaa gtgacaagct gctttccaga ctccacggc				859
ccggctgctt ttatggccct gcttcacagg gagaagagtg gagcacaggc gtaacccct				919
cagtctggga ggtcactgcc ccaggacctg gaccttttag agagctctct cggccatctt				979
tatctcccag agctgccatc taacaattgt caaggaacct catgtctcac ctcaggggcc				1039
agggtactct ctcacttaac caccctggtc aagtgagcat cttctggctg gctgtctccc				1099
ctcactatga aaacccccaaa cttctaccaa taacgggatt tgggttctgt tatgataact				1159
gtgacacacaca cacacactca cactctgata aaagagatgg agacactaaa aaaaaaaaaaa				1219
aaaaaaaaaaaa aaaaaaaaaaa aaa				1242

<210> 17
<211> 207
<212> PRT
<213> mVRF

```

<400> 17
Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Val Ala Leu Leu Gln Leu
      1           5           10          15
Ala Arg Thr Gln Ala Pro Val Ser Gln Phe Asp Gly Pro Ser His Gln
      20          25          30
Lys Lys Val Val Pro Trp Ile Asp Val Tyr Ala Arg Ala Thr Cys Gln
      35          40          45
Pro Arg Glu Val Val Val Pro Leu Ser Met Glu Leu Met Gly Asn Val
      50          55          60
Val Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
      65          70          75          80
Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
      85          90          95
Val Arg Met Gln Ile Leu Met Ile Gln Tyr Pro Ser Ser Gln Leu Gly
      100         105         110
Glu Met Ser Leu Gly Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
      115         120         125
Lys Glu Ser Ala Val Arg Pro Asp Arg Val Ala Ile Pro His His Arg
      130         135         140

```

Pro	Gln	Pro	Arg	Ser	Val	Pro	Gly	Trp	Asp	Ser	Thr	Pro	Gly	Ala	Pro
145					150					155					160
Ser	Pro	Ala	Asp	Ile	Ile	His	Pro	Thr	Pro	Ala	Pro	Gly	Ser	Ser	Ala
					165					170					175
Arg	Leu	Ala	Pro	Ser	Ala	Ala	Asn	Ala	Leu	Thr	Pro	Gly	Pro	Ala	Val
					180					185					190
Ala	Ala	Val	Asp	Ala	Ala	Ala	Ser	Ser	Ile	Ala	Lys	Gly	Gly	Ala	
					195					200					205

<210> 18

<211> 188

<212> PRT

<213> mVRF167

<400> 18

Met	Ser	Pro	Leu	Leu	Arg	Arg	Leu	Leu	Leu	Val	Ala	Leu	Leu	Gln	Leu
1					5					10					15

Ala	Arg	Thr	Gln	Ala	Pro	Val	Ser	Gln	Phe	Asp	Gly	Pro	Ser	His	Gln
					20				25						30

Lys	Lys	Val	Val	Pro	Trp	Ile	Asp	Val	Tyr	Ala	Arg	Ala	Thr	Cys	Gln
					35			40							45

Pro	Arg	Glu	Val	Val	Val	Pro	Leu	Ser	Met	Glu	Leu	Met	Gly	Asn	Val
						50		55				60			

Val	Lys	Gln	Leu	Val	Pro	Ser	Cys	Val	Thr	Val	Gln	Arg	Cys	Gly	
					65		70			75					80

Cys	Cys	Pro	Asp	Asp	Gly	Leu	Glu	Cys	Val	Pro	Thr	Gly	Gln	His	Gln
					85				90					95	

Val	Arg	Met	Gln	Ile	Leu	Met	Ile	Gln	Tyr	Pro	Ser	Ser	Gln	Leu	Gly
					100				105						110

Glu	Met	Ser	Leu	Gly	Glu	His	Ser	Gln	Cys	Glu	Cys	Arg	Pro	Lys	Lys
						115		120				125			

Lys	Glu	Ser	Ala	Val	Arg	Pro	Asp	Ser	Pro	Arg	Ile	Leu	Cys	Pro	Pro
					130		135				140				

Cys	Thr	Gln	Arg	Arg	Gln	Arg	Pro	Asp	Pro	Arg	Thr	Cys	Arg	Cys	Arg
					145		150			155					160

Cys	Arg	Arg	Arg	Arg	Phe	Leu	His	Cys	Gln	Gly	Arg	Gly	Leu	Glu	Leu
					165				170						175

Asn	Pro	Asp	Thr	Cys	Arg	Cys	Arg	Lys	Pro	Arg	Lys				
					180			185							

<210> 19

<211> 188

<212> PRT
<213> hVRF167

<400> 19

Met Ser Pro Leu Leu Arg Arg Leu Leu Ala Ala Leu Leu Gln Leu
1 5 10 15

Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
20 25 30

Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
35 40 45

Pro Arg Glu Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
50 55 60

Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
65 70 75 80

Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
85 90 95

Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
100 105 110

Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
115 120 125

Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro Arg
130 135 140

Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys Arg
145 150 155 160

Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu Leu
165 170 175

Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg
180 185

<210> 20

<211> 71

<212> PRT

<213> mVRF186

<400> 20

Arg Val Ala Ile Pro His His Arg Pro Gln Pro Arg Ser Val Pro Gly
1 5 10 15

Trp Asp Ser Thr Pro Gly Ala Pro Ser Pro Ala Asp Ile Ile His Pro
20 25 30

Thr Pro Ala Pro Gly Ser Ser Ala Arg Leu Ala Pro Ser Ala Ala Asn
35 40 45

Ala Leu Thr Pro Gly Pro Ala Val Ala Ala Val Asp Ala Ala Ala Ser
50 55 60

Ser Ile Ala Lys Gly Gly Ala
65 70

<210> 21
<211> 71
<212> PRT
<213> hVRF186

<400> 21
Arg Ala Ala Thr Pro His His Arg Pro Gln Pro Arg Ser Val Pro Gly
1 5 10 15

Trp Asp Ser Ala Pro Gly Ala Pro Ser Pro Ala Asp Ile Thr His Pro
20 25 30

Thr Pro Ala Pro Gly Pro Ser Ala His Ala Ala Pro Ser Thr Thr Ser
35 40 45

Ala Leu Thr Pro Gly Pro Ala Ala Ala Ala Asp Ala Ala Ala Ser
50 55 60

Ser Val Ala Lys Gly Gly Ala
65 70

<210> 22
<211> 214
<212> PRT
<213> mVEGF188

<400> 22
Met Asn Phe Leu Leu Ser Trp Val His Trp Thr Leu Ala Leu Leu Leu
1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Thr Thr Glu Gly
20 25 30

Glu Gln Lys Ser His Glu Val Ile Lys Phe Met Asp Val Tyr Gln Arg
35 40 45

Ser Tyr Cys Arg Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu Tyr
50 55 60

Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu Met
65 70 75 80

Arg Cys Ala Gly Cys Cys Asn Asp Glu Ala Leu Glu Cys Val Pro Thr
85 90 95

Ser Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His Gln
100 105 110

Ser Gln His Ile Gly Glu Met Ser Phe Leu Gln His Ser Arg Cys Glu
115 120 125

Cys Arg Pro Lys Lys Asp Arg Thr Lys Pro Glu Lys Lys Ser Val Arg
130 135 140

Gly Lys Gly Lys Gly Gln Lys Arg Lys Arg Lys Lys Ser Arg Phe Lys
145 150 155 160

Ser Trp Ser Val His Cys Glu Pro Cys Ser Glu Arg Arg Lys His Leu
165 170 175

Phe Val Gln Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr Asp
180 185 190

Ser Arg Cys Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys Arg
195 200 205

C
Cont
Cys Asp Lys Pro Arg Arg
210